

last 24 amino acids (SEQ ID NO:17) of the FLT15 clone, are divergent from the wild type FLT sequence.

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#          SEQUENCE LISTING
- (1) GENERAL INFORMATION:
-   (iii) NUMBER OF SEQUENCES: 17
- (2) INFORMATION FOR SEQ ID NO:1:
-   (i) SEQUENCE CHARACTERISTICS:
#acids      (A) LENGTH: 976 amino
              (B) TYPE: amino acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear
-   (ii) MOLECULE TYPE: protein
-   (iii) HYPOTHETICAL: NO
-   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
- Met Arg Gly Ala Arg Gly Ala Trp Asp Phe Le - #u Cys Val Leu Leu Leu
#          15
- Leu Leu Arg Val Gln Thr Gly Ser Ser Gln Pr - #o Ser Val Ser Pro Gly
#          30
- Glu Pro Ser Pro Pro Ser Ile His Pro Gly Ly - #s Ser Asp Leu Ile Val
#          45
- Arg Val Gly Asp Glu Ile Arg Leu Leu Cys Th - #r Asp Pro Gly Phe Val
#          60
- Lys Trp Thr Phe Glu Ile Leu Asp Glu Thr As - #n Glu Asn Lys Gln Asn
#80
- Glu Trp Ile Thr Glu Lys Ala Glu Ala Thr As - #n Thr Gly Lys Tyr Thr
#          95
- Cys Thr Asn Lys His Gly Leu Ser Asn Ser Il - #e Tyr Val Phe Val Arg
#          110
- Asp Pro Ala Lys Leu Phe Leu Val Asp Arg Se - #r Leu Tyr Gly Lys Glu
#          125
- Asp Asn Asp Thr Leu Val Arg Cys Pro Leu Th - #r Asp Pro Glu Val Thr
#          140
- Asn Tyr Ser Leu Lys Gly Cys Gln Gly Lys Pr - #o Leu Pro Lys Asp Leu
145          1 - #50          1 - #55          1 -
#60
- Arg Phe Ile Pro Asp Pro Lys Ala Gly Ile Me - #t Ile Lys Ser Val Lys
#          175
- Arg Ala Tyr His Arg Leu Cys Leu His Cys Se - #r Val Asp Gln Glu Gly
#          190
- Lys Ser Val Leu Ser Glu Lys Phe Ile Leu Ly - #s Val Arg Pro Ala Phe
#          205
- Lys Ala Val Pro Val Val Ser Val Ser Lys Al - #a Ser Tyr Leu Leu Arg
#          220
- Glu Gly Glu Glu Phe Thr Val Thr Cys Thr Il - #e Lys Asp Val Ser Ser
225          2 - #30          2 - #35          2 -
#40
- Ser Val Tyr Ser Thr Trp Lys Arg Glu Asn Se - #r Gln Thr Lys Leu Gln
#          255
- Glu Lys Tyr Asn Ser Trp His His Gly Asp Ph - #e Asn Tyr Glu Arg Gln
#          270
- Ala Thr Leu Thr Ile Ser Ser Ala Arg Val As - #n Asp Ser Gly Val Phe
#          285
- Met Cys Tyr Ala Asn Asn Thr Phe Gly Ser Al - #a Asn Val Thr Thr Thr
#          300

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- Leu Glu Val Val Asp Lys Gly Phe Ile Asn Il - #e Phe Pro Met Ile Asn
 305 3 - #10 3 - #15 3 -
 #20
 - Thr Thr Val Phe Val Asn Asp Gly Glu Asn Va - #l Asp Leu Ile Val Glu
 # 335
 - Tyr Glu Ala Phe Pro Lys Pro Glu His Gln Gl - #n Trp Ile Tyr Met Asn
 # 350
 - Arg Thr Phe Thr Asp Lys Trp Glu Asp Tyr Pr - #o Lys Ser Glu Asn Glu
 # 365
 - Ser Asn Ile Arg Tyr Val Ser Glu Leu His Le - #u Thr Arg Leu Lys Gly
 # 380
 - Thr Glu Gly Gly Thr Tyr Thr Phe Leu Val Se - #r Asn Ser Asp Val Asn
 385 3 - #90 3 - #95 4 -
 #00
 - Ala Ala Ile Ala Phe Asn Val Tyr Val Asn Th - #r Lys Pro Glu Ile Leu
 # 415
 - Thr Tyr Asp Arg Leu Val Asn Gly Met Leu Gl - #n Cys Val Ala Ala Gly
 # 430
 - Phe Pro Glu Pro Thr Ile Asp Trp Tyr Phe Cy - #s Pro Gly Thr Glu Gln
 # 445
 - Arg Cys Ser Ala Ser Val Leu Pro Val Asp Va - #l Gln Thr Leu Asn Ser
 # 460
 - Ser Gly Pro Pro Phe Gly Lys Leu Val Val Gl - #n Ser Ser Ile Asp Ser
 465 4 - #70 4 - #75 4 -
 #80
 - Ser Ala Phe Lys His Asn Gly Thr Val Glu Cy - #s Lys Ala Tyr Asn Asp
 # 495
 - Val Gly Lys Thr Ser Ala Tyr Phe Asn Phe Al - #a Phe Lys Gly Asn Asn
 # 510
 - Lys Glu Gln Ile His Pro His Thr Leu Phe Th - #r Pro Leu Leu Ile Gly
 # 525
 - Phe Val Ile Val Ala Gly Met Met Cys Ile Il - #e Val Met Ile Leu Thr
 # 540
 - Tyr Lys Tyr Leu Gln Lys Pro Met Tyr Glu Va - #l Gln Trp Lys Val Val
 545 5 - #50 5 - #55 5 -
 #60
 - Glu Glu Ile Asn Gly Asn Asn Tyr Val Tyr Il - #e Asp Pro Thr Gln Leu
 # 575
 - Pro Tyr Asp His Lys Trp Glu Phe Pro Arg As - #n Arg Leu Ser Phe Gly
 # 590
 - Lys Thr Leu Gly Ala Gly Ala Phe Gly Lys Va - #l Val Glu Ala Thr Ala
 # 605
 - Tyr Gly Leu Ile Lys Ser Asp Ala Ala Met Th - #r Val Ala Val Lys Met
 # 620
 - Leu Lys Pro Ser Ala His Leu Thr Glu Arg Gl - #u Ala Leu Met Ser Glu
 625 6 - #30 6 - #35 6 -
 #40
 - Leu Lys Val Leu Ser Tyr Leu Gly Asn His Me - #t Asn Ile Val Asn Leu
 # 655
 - Leu Gly Ala Cys Thr Ile Gly Gly Pro Thr Le - #u Val Ile Thr Glu Tyr
 # 670
 - Cys Cys Tyr Gly Asp Leu Leu Asn Phe Leu Ar - #g Arg Lys Arg Asp Ser
 # 685
 - Phe Ile Cys Ser Lys Gln Glu Asp His Ala Gl - #u Ala Ala Leu Tyr Lys
 # 700
 - Asn Leu Leu His Ser Lys Glu Ser Ser Cys Se - #r Asp Ser Thr Asn Glu
 705 7 - #10 7 - #15 7 -

#20
 - Tyr Met Asp Met Lys Pro Gly Val Ser Tyr Va - #l Val Pro Thr Lys Ala
 # 735
 - Asp Lys Arg Arg Ser Val Arg Ile Gly Ser Ty - #r Ile Glu Arg Asp Val
 # 750
 - Thr Pro Ala Ile Met Glu Asp Asp Glu Leu Al - #a Leu Asp Leu Glu Asp
 # 765
 - Leu Leu Ser Phe Ser Tyr Gln Val Ala Lys Gl - #y Met Ala Phe Leu Ala
 # 780
 - Ser Lys Asn Cys Ile His Arg Asp Leu Ala Al - #a Arg Asn Ile Leu Leu
 785 7 - #90 7 - #95 8 -
 #00
 - Thr His Gly Arg Ile Thr Lys Ile Cys Asp Ph - #e Gly Leu Ala Arg Asp
 # 815
 - Ile Lys Asn Asp Ser Asn Tyr Val Val Lys Gl - #y Asn Ala Arg Leu Pro
 # 830
 - Val Lys Trp Met Ala Pro Glu Ser Ile Phe As - #n Cys Val Tyr Thr Phe
 # 845
 - Glu Ser Asp Val Trp Ser Tyr Gly Ile Phe Le - #u Trp Glu Leu Phe Ser
 # 860
 - Leu Gly Ser Ser Pro Tyr Pro Gly Met Pro Va - #l Asp Ser Lys Phe Tyr
 865 8 - #70 8 - #75 8 -
 #80
 - Lys Met Ile Lys Glu Gly Phe Arg Met Leu Se - #r Pro Glu His Ala Pro
 # 895
 - Ala Glu Met Tyr Asp Ile Met Lys Thr Cys Tr - #p Asp Ala Asp Pro Leu
 # 910
 - Lys Arg Pro Thr Phe Lys Gln Ile Val Gln Le - #u Ile Glu Lys Gln Ile
 # 925
 - Ser Glu Ser Thr Asn His Ile Tyr Ser Asn Le - #u Ala Asn Cys Ser Pro
 # 940
 - Asn Arg Gln Lys Pro Val Val Asp His Ser Va - #l Arg Ile Asn Ser Val
 945 9 - #50 9 - #55 9 -
 #60
 - Gly Ser Thr Ala Ser Ser Ser Gln Pro Leu Le - #u Val His Asp Asp Val
 # 975
 - (2) INFORMATION FOR SEQ ID NO:2:
 - (i) SEQUENCE CHARACTERISTICS:
 #acids (A) LENGTH: 972 amino
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (iii) HYPOTHETICAL: NO
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
 - Met Gly Pro Gly Val Leu Leu Leu Leu Leu Va - #l Ala Thr Ala Trp His
 # 15
 - Gly Gln Gly Ile Pro Val Ile Glu Pro Ser Va - #l Pro Glu Leu Val Val
 # 30
 - Lys Pro Gly Ala Thr Val Thr Leu Arg Cys Va - #l Gly Asn Gly Ser Val
 # 45
 - Glu Trp Asp Gly Pro Pro Ser Pro His Trp Th - #r Leu Tyr Ser Asp Gly
 # 60
 - Ser Ser Ser Ile Leu Ser Thr Asn Asn Ala Th - #r Phe Gln Asn Thr Gly
 #80
 - Thr Tyr Arg Cys Thr Glu Pro Gly Asp Pro Le - #u Gly Gly Ser Ala Ala
 # 95

- Ile His Leu Tyr Val Lys Asp Pro Ala Arg Pr - #o Trp Asn Val Leu Ala
 # 110
 - Gln Glu Val Val Val Phe Glu Asp Gln Asp Al - #a Leu Leu Pro Cys Leu
 # 125
 - Leu Thr Asp Pro Val Leu Glu Ala Gly Val Se - #r Leu Val Arg Val Arg
 # 140
 - Gly Arg Pro Leu Met Arg His Thr Asn Tyr Se - #r Phe Ser Pro Trp His
 145 1 - #50 1 - #55 1 -
 #60
 - Gly Phe Thr Ile His Arg Ala Lys Phe Ile Gl - #n Ser Gln Asp Tyr Gln
 # 175
 - Cys Ser Ala Leu Met Gly Gly Arg Lys Val Me - #t Ser Ile Ser Ile Arg
 # 190
 - Leu Lys Val Gln Lys Val Ile Pro Gly Pro Pr - #o Ala Leu Thr Leu Val
 # 205
 - Pro Ala Glu Leu Val Arg Ile Arg Gly Glu Al - #a Ala Gln Ile Val Cys
 # 220
 - Ser Ala Ser Ser Val Asp Val Asn Phe Asp Va - #l Phe Leu Gln His Asn
 225 2 - #30 2 - #35 2 -
 #40
 - Asn Thr Lys Leu Ala Ile Pro Gln Gln Ser As - #p Phe His Asn Asn Arg
 # 255
 - Tyr Gln Lys Val Leu Thr Leu Asn Leu Asp Gl - #n Val Asp Phe Gln His
 # 270
 - Ala Gly Asn Tyr Ser Cys Val Ala Ser Asn Va - #l Gln Gly Lys His Ser
 # 285
 - Thr Ser Met Phe Phe Arg Val Val Glu Ser Al - #a Tyr Leu Asn Leu Ser
 # 300
 - Ser Glu Gln Asn Leu Ile Gln Glu Val Thr Va - #l Gly Glu Gly Leu Asn
 305 3 - #10 3 - #15 3 -
 #20
 - Leu Lys Val Met Val Glu Ala Tyr Pro Gly Le - #u Gln Gly Phe Asn Trp
 # 335
 - Thr Tyr Leu Gly Pro Phe Ser Asp His Gln Pr - #o Glu Pro Lys Leu Ala
 # 350
 - Asn Ala Thr Thr Lys Asp Thr Tyr Arg His Th - #r Phe Thr Leu Ser Leu
 # 365
 - Pro Arg Leu Lys Pro Ser Glu Ala Gly Arg Ty - #r Ser Phe Leu Ala Arg
 # 380
 - Asn Pro Gly Gly Trp Arg Ala Leu Thr Phe Gl - #u Leu Thr Leu Arg Tyr
 385 3 - #90 3 - #95 4 -
 #00
 - Pro Pro Glu Val Ser Val Ile Trp Thr Phe Il - #e Asn Gly Ser Gly Thr
 # 415
 - Leu Leu Cys Ala Ala Ser Gly Tyr Pro Gln Pr - #o Asn Val Thr Trp Leu
 # 430
 - Gln Cys Ser Gly His Thr Asp Arg Cys Asp Gl - #u Ala Gln Val Leu Gln
 # 445
 - Val Trp Asp Asp Pro Tyr Pro Glu Val Leu Se - #r Gln Glu Pro Phe His
 # 460
 - Lys Val Thr Val Gln Ser Leu Leu Thr Val Gl - #u Thr Leu Glu His Asn
 465 4 - #70 4 - #75 4 -
 #80
 - Gln Thr Tyr Glu Cys Arg Ala His Asn Ser Va - #l Gly Ser Gly Ser Trp
 # 495
 - Ala Phe Ile Pro Ile Ser Ala Gly Ala His Th - #r His Pro Pro Asp Glu
 # 510

- Phe Leu Phe Thr Pro Val Val Val Ala Cys Me - #t Ser Ile Met Ala Leu
 # 525
 - Leu Leu Leu Leu Leu Leu Leu Leu Tyr Ly - #s Tyr Lys Gln Lys Pro
 # 540
 - Lys Tyr Gln Val Arg Trp Lys Ile Ile Glu Se - #r Tyr Glu Gly Asn Ser
 545 5 - #50 5 - #55 5 -
 #60
 - Tyr Thr Phe Ile Asp Pro Thr Gln Leu Pro Ty - #r Asn Glu Lys Trp Glu
 # 575
 - Phe Pro Arg Asn Asn Leu Gln Phe Gly Lys Th - #r Leu Gly Ala Gly Ala
 # 590
 - Phe Gly Lys Val Val Glu Ala Thr Ala Phe Gl - #y Leu Gly Lys Glu Asp
 # 605
 - Ala Val Leu Lys Val Ala Val Lys Met Leu Ly - #s Ser Thr Ala His Ala
 # 620
 - Asp Glu Lys Glu Ala Leu Met Ser Glu Leu Ly - #s Ile Met Ser His Leu
 625 6 - #30 6 - #35 6 -
 #40
 - Gly Gln His Glu Asn Ile Val Asn Leu Leu Gl - #y Ala Cys Thr His Gly
 # 655
 - Gly Pro Val Leu Val Ile Thr Glu Tyr Cys Cy - #s Tyr Gly Asp Leu Leu
 # 670
 - Asn Phe Leu Arg Arg Lys Ala Glu Ala Met Le - #u Gly Pro Ser Leu Ser
 # 685
 - Pro Gly Gln Asp Pro Glu Gly Gly Val Asp Ty - #r Lys Asn Ile His Leu
 # 700
 - Glu Lys Lys Tyr Val Arg Arg Asp Ser Gly Ph - #e Ser Ser Gln Gly Val
 705 7 - #10 7 - #15 7 -
 #20
 - Asp Thr Tyr Val Glu Met Arg Pro Val Ser Th - #r Ser Ser Asn Asp Ser
 # 735

 - Phe Ser Glu Gln Asp Leu Asp Lys Glu Asp Gl - #y Arg Pro Leu Glu Leu
 # 750
 - Arg Asp Leu Leu His Phe Ser Ser Gln Val Al - #a Gln Gly Met Ala Phe
 # 765
 - Leu Ala Ser Lys Asn Cys Ile His Arg Asp Va - #l Ala Ala Arg Asn Val
 # 780
 - Leu Leu Thr Asn Gly His Val Ala Lys Ile Gl - #y Asp Phe Gly Leu Ala
 785 7 - #90 7 - #95 8 -
 #00
 - Arg Asp Ile Met Asn Asp Ser Asn Tyr Ile Va - #l Lys Gly Asn Ala Arg
 # 815
 - Leu Pro Val Lys Trp Met Ala Pro Glu Ser Il - #e Phe Asp Cys Val Tyr
 # 830
 - Thr Val Gln Ser Asp Val Trp Ser Tyr Gly Il - #e Leu Leu Trp Glu Ile
 # 845
 - Phe Ser Leu Gly Leu Asn Pro Tyr Pro Gly Il - #e Leu Val Asn Ser Lys
 # 860
 - Phe Tyr Lys Leu Val Lys Asp Gly Tyr Gln Me - #t Ala Gln Pro Ala Phe
 865 8 - #70 8 - #75 8 -
 #80
 - Ala Pro Lys Asn Ile Tyr Ser Ile Met Gln Al - #a Cys Trp Ala Leu Glu
 # 895
 - Pro Thr His Arg Pro Thr Phe Gln Gln Ile Cy - #s Ser Phe Leu Gln Glu
 # 910

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- Gln Ala Gln Glu Asp Arg Arg Glu Arg Asp Ty - #r Thr Asn Leu Pro Ser
#      925
- Ser Ser Arg Ser Gly Gly Ser Gly Ser Ser Se - #r Ser Glu Leu Glu Glu
#      940
- Glu Ser Ser Ser Glu His Leu Thr Cys Cys Gl - #u Gln Gly Asp Ile Ala
945      9 - #50      9 - #55      9 -
#60
- Gln Pro Leu Leu Gln Pro Asn Asn Tyr Gln Ph - #e Cys
#      970
- (2) INFORMATION FOR SEQ ID NO:3:
- (i) SEQUENCE CHARACTERISTICS:
#acids (A) LENGTH: 1338 amino
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
- Met Val Ser Tyr Trp Asp Thr Gly Val Leu Le - #u Cys Ala Leu Leu Ser
#      15
- Cys Leu Leu Leu Thr Gly Ser Ser Ser Gly Se - #r Lys Leu Lys Asp Pro
#      30
- Glu Leu Ser Leu Lys Gly Thr Gln His Ile Me - #t Gln Ala Gly Gln Thr
#      45
- Leu His Leu Gln Cys Arg Gly Glu Ala Ala Hi - #s Lys Trp Ser Leu Pro
#      60
- Glu Met Val Ser Lys Glu Ser Glu Arg Leu Se - #r Ile Thr Lys Ser Ala
#80
- Cys Gly Arg Asn Gly Lys Gln Phe Cys Ser Th - #r Leu Thr Leu Asn Thr
#      95
- Ala Gln Ala Asn His Thr Gly Phe Tyr Ser Cy - #s Lys Tyr Leu Ala Val
#      110
- Pro Thr Ser Lys Lys Lys Glu Thr Glu Ser Al - #a Ile Tyr Ile Phe Ile
#      125
- Ser Asp Thr Gly Arg Pro Phe Val Glu Met Ty - #r Ser Glu Ile Pro Glu
#      140
- Ile Ile His Met Thr Glu Gly Arg Glu Leu Va - #l Ile Pro Cys Arg Val
145      1 - #50      1 - #55      1 -
#60
- Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Ly - #s Phe Pro Leu Asp Thr
#      175
- Leu Ile Pro Asp Gly Lys Arg Ile Ile Trp As - #p Ser Arg Lys Gly Phe
#      190
- Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile Gl - #y Leu Leu Thr Cys Glu
#      205
- Ala Thr Val Asn Gly His Leu Tyr Lys Thr As - #n Tyr Leu Thr His Arg
#      220
- Gln Thr Asn Thr Ile Ile Asp Val Gln Ile Se - #r Thr Pro Arg Pro Val
225      2 - #30      2 - #35      2 -
#40
- Lys Leu Leu Arg Gly His Thr Leu Val Leu As - #n Cys Thr Ala Thr Thr
#      255
- Pro Leu Asn Thr Arg Val Gln Met Thr Trp Se - #r Tyr Pro Asp Glu Lys
#      270
- Asn Lys Arg Ala Ser Val Arg Arg Arg Ile As - #p Gln Ser Asn Ser His
#      285
- Ala Asn Ile Phe Tyr Ser Val Leu Thr Ile As - #p Lys Met Gln Asn Lys

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# 300
- Asp Lys Gly Leu Tyr Thr Cys Arg Val Arg Se - #r Gly Pro Ser Phe Lys
305          3 - #10          3 - #15          3 -
#20
- Ser Val Asn Thr Ser Val His Ile Tyr Asp Ly - #s Ala Phe Ile Thr Val
#          335
- Lys His Arg Lys Gln Gln Val Leu Glu Thr Va - #l Ala Gly Lys Arg Ser
#          350
- Tyr Arg Leu Ser Met Lys Val Lys Ala Phe Pr - #o Ser Pro Glu Val Val
#          365
- Trp Leu Lys Asp Gly Leu Pro Ala Thr Glu Ly - #s Ser Ala Arg Tyr Leu
# 380
- Thr Arg Gly Tyr Ser Leu Ile Ile Lys Asp Va - #l Thr Glu Glu Asp Ala
385          3 - #90          3 - #95          4 -
#00
- Gly Asn Tyr Thr Ile Leu Leu Ser Ile Lys Gl - #n Ser Asn Val Phe Lys
#          415
- Asn Leu Thr Ala Thr Leu Ile Val Asn Val Ly - #s Pro Gln Ile Tyr Glu
#          430
- Lys Ala Val Ser Ser Phe Pro Asp Pro Ala Le - #u Tyr Pro Leu Gly Ser
#          445
- Arg Gln Ile Leu Thr Cys Thr Ala Tyr Gly Il - #e Pro Gln Pro Thr Ile
# 460
- Lys Trp Phe Trp His Pro Cys Asn His Asn Hi - #s Ser Glu Ala Arg Cys
465          4 - #70          4 - #75          4 -
#80
- Asp Phe Cys Ser Asn Asn Glu Glu Ser Phe Il - #e Leu Asp Ala Asp Ser
#          495
- Asn Met Gly Asn Arg Ile Glu Ser Ile Thr Gl - #n Arg Met Ala Ile Ile
#          510
- Glu Gly Lys Asn Lys Met Ala Ser Thr Leu Va - #l Val Ala Asp Ser Arg
#          525
- Ile Ser Gly Ile Tyr Ile Cys Ile Ala Ser As - #n Lys Val Gly Thr Val
# 540
- Gly Arg Asn Ile Ser Phe Tyr Ile Thr Asp Va - #l Pro Asn Gly Phe His
545          5 - #50          5 - #55          5 -
#60
- Val Asn Leu Glu Lys Met Pro Thr Glu Gly Gl - #u Asp Leu Lys Leu Ser
#          575
- Cys Thr Val Asn Lys Phe Leu Tyr Arg Asp Va - #l Thr Trp Ile Leu Leu
#          590
- Arg Thr Val Asn Asn Arg Thr Met His Tyr Se - #r Ile Ser Lys Gln Lys
#          605
- Met Ala Ile Thr Lys Glu His Ser Ile Thr Le - #u Asn Leu Thr Ile Met
# 620
- Asn Val Ser Leu Gln Asp Ser Gly Thr Tyr Al - #a Cys Arg Ala Arg Asn
625          6 - #30          6 - #35          6 -
#40
- Val Tyr Thr Gly Glu Glu Ile Leu Gln Lys Ly - #s Glu Ile Thr Ile Arg
#          655
- Asp Gln Glu Ala Pro Tyr Leu Leu Arg Asn Le - #u Ser Asp His Thr Val
#          670
- Ala Ile Ser Ser Ser Thr Thr Leu Asp Cys Hi - #s Ala Asn Gly Val Pro
#          685
- Glu Pro Gln Ile Thr Trp Phe Lys Asn Asn Hi - #s Lys Ile Gln Gln Glu
# 700
- Pro Gly Ile Ile Leu Gly Pro Gly Ser Ser Th - #r Leu Phe Ile Glu Arg

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705 7 - #10 7 - #15 7 -
 #20
 - Val Thr Glu Glu Asp Glu Gly Val Tyr His Cy - #s Lys Ala Thr Asn Gln
 # 735
 - Lys Gly Ser Val Glu Ser Ser Ala Tyr Leu Th - #r Val Gln Gly Thr Ser
 # 750
 - Asp Lys Ser Asn Leu Glu Leu Ile Thr Leu Th - #r Cys Thr Cys Val Ala
 # 765
 - Ala Thr Leu Phe Trp Leu Leu Leu Thr Leu Le - #u Ile Arg Lys Met Lys
 # 780
 - Arg Ser Ser Ser Glu Ile Lys Thr Asp Tyr Le - #u Ser Ile Ile Met Asp
 785 7 - #90 7 - #95 8 -
 #00
 - Pro Asp Glu Val Pro Leu Asp Glu Gln Cys Gl - #u Arg Leu Pro Tyr Asp
 # 815
 - Ala Ser Lys Trp Glu Phe Ala Arg Glu Arg Le - #u Lys Leu Gly Lys Ser
 # 830
 - Leu Gly Arg Gly Ala Phe Gly Lys Val Val Gl - #n Ala Ser Ala Phe Gly
 # 845
 - Ile Lys Lys Ser Pro Thr Cys Arg Thr Val Al - #a Val Lys Met Leu Lys
 # 860
 - Glu Gly Ala Thr Ala Ser Glu Tyr Lys Ala Le - #u Met Thr Glu Leu Lys
 865 8 - #70 8 - #75 8 -
 #80
 - Ile Leu Thr His Ile Gly His His Leu Asn Va - #l Val Asn Leu Leu Gly
 # 895
 - Ala Cys Thr Lys Gln Gly Gly Pro Leu Met Va - #l Ile Val Glu Tyr Cys
 # 910
 - Lys Tyr Gly Asn Leu Ser Asn Tyr Leu Lys Se - #r Lys Arg Asp Leu Phe
 # 925
 - Phe Leu Asn Lys Asp Ala Ala Leu His Met Gl - #u Pro Lys Lys Glu Lys
 # 940
 - Met Glu Pro Gly Leu Glu Gln Gly Lys Lys Pr - #o Arg Leu Asp Ser Val
 945 9 - #50 9 - #55 9 -
 #60
 - Thr Ser Ser Glu Ser Phe Ala Ser Ser Gly Ph - #e Gln Glu Asp Lys Ser
 # 975
 - Leu Ser Asp Val Glu Glu Glu Glu Asp Ser As - #p Gly Phe Tyr Lys Glu
 # 990
 - Pro Ile Thr Met Glu Asp Leu Ile Ser Tyr Se - #r Phe Gln Val Ala Arg
 # 10050
 - Gly Met Glu Phe Leu Ser Ser Arg Lys Cys Il - #e His Arg Asp Leu Ala
 # 10205
 - Ala Arg Asn Ile Leu Leu Ser Glu Asn Asn Va - #l Val Lys Ile Cys Asp
 # 10401030 - # 1035
 - Phe Gly Leu Ala Arg Asp Ile Tyr Lys Asn Pr - #o Asp Tyr Val Arg Lys
 # 10550
 - Gly Asp Thr Arg Leu Pro Leu Lys Trp Met Al - #a Pro Glu Ser Ile Phe
 # 10705
 - Asp Lys Ile Tyr Ser Thr Lys Ser Asp Val Tr - #p Ser Tyr Gly Val Leu
 # 10850
 - Leu Trp Glu Ile Phe Ser Leu Gly Gly Ser Pr - #o Tyr Pro Gly Val Gln
 # 11005
 - Met Asp Glu Asp Phe Cys Ser Arg Leu Arg Gl - #u Gly Met Arg Met Arg
 # 11201110 - # 1115
 - Ala Pro Glu Tyr Ser Thr Pro Glu Ile Tyr Gl - #n Ile Met Leu Asp Cys
 # 11350

- Trp His Arg Asp Pro Lys Glu Arg Pro Arg Ph - #e Ala Glu Leu Val Glu
11505

- Lys Leu Gly Asp Leu Leu Gln Ala Asn Val Gl - #n Gln Asp Gly Lys Asp
11650

- Tyr Ile Pro Ile Asn Ala Ile Leu Thr Gly As - #n Ser Gly Phe Thr Tyr
11805

- Ser Thr Pro Ala Phe Ser Glu Asp Phe Phe Ly - #s Glu Ser Ile Ser Ala
12001190 - # 1195

- Pro Lys Phe Asn Ser Gly Ser Ser Asp Asp Va - #l Arg Tyr Val Asn Ala
12150

- Phe Lys Phe Met Ser Leu Glu Arg Ile Lys Th - #r Phe Glu Glu Leu Leu
12305

- Pro Asn Ala Thr Ser Met Phe Asp Asp Tyr Gl - #n Gly Asp Ser Ser Thr
12450

- Leu Leu Ala Ser Pro Met Leu Lys Arg Phe Th - #r Trp Thr Asp Ser Lys
12605

- Pro Lys Ala Ser Leu Lys Ile Asp Leu Arg Va - #l Thr Ser Lys Ser Lys
12801270 - # 1275

- Glu Ser Gly Leu Ser Asp Val Ser Arg Pro Se - #r Phe Cys His Ser Ser
12950

- Cys Gly His Val Ser Glu Gly Lys Arg Arg Ph - #e Thr Tyr Asp His Ala
13105

- Glu Leu Glu Arg Lys Ile Ala Cys Cys Ser Pr - #o Pro Pro Asp Tyr Asn
13250

- Ser Val Val Leu Tyr Ser Thr Pro Pro Ile
1335

- (2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:

#pairs (A) LENGTH: 398 base
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

- AGAGTGC GCC AACGAGCCCA GCCAAGCTGT CTCAGTGACA AACCCATACC CT - #TGTGAAGA
60

- ATGGAGAAGT GTGGAGGACT TCCAGGGAGG AAATAAAATT GAAGTTAATA AA - #AATCAATT
120

- TGCTCTAATT GAAGGAAAAA ACAAACTGT AAGTACCCTT GTTATCCAAG CG - #GCAAATGT
180

- GTCAGCTTTG TACAAATGTG AAGCGGTCAA CAAAGTCGGG AGAGGAGAGA GG - #GTGATCTC
240

- CTTCCACGTG ACCAGGGGTC CTGAAATTAC TTTGCAACCT GACATGCAGC CC - #ACTGAGCA
300

- GGAGAGCGTG TCTTTGTGGT GCACTGCAGA CAGATCTACG TTTGAGAACC TC - #ACATGGTA
360

398 CCTC TGCCAATCCA TGTGGGAG

- (2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:

#pairs (A) LENGTH: 551 base
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

- ACCCCTGTAA CCATAATCAT TCCGAAGCAA GGTGTGACTT TTGTTCCAAT AA - #TGAAGAGT
60
- CCTTTATCCT GGATGCTGAC AGCAACATGG GAAACAGAAT TGAGAGCATC AC - #TCAGCGCA

120
- TGGCAATAAT AGAAGGAAAG AATAAGATGG CTAGCACCTT GGTGTGGCT GA - #CTCTAGAA
180
- TTTCTGGAAT CTACATTTGC ATAGCTTCCA ATAAAGTTGG GACTGTGGGA AG - #AAACATAA
240
- GCTTTTATAT CACAGATGTG CCAAATGGGT TTCATGTTAA CTTGGAAAAA AT - #GCCGACGG
300
- AAGGAGAGGA CCTGAAACTG TCTTGCACAG TTAACAAGTT CTTATACAGA GA - #CGTTACTT
360
- GGATTTTACT GCGGACAGTT AATAACAGAA CAATGCACTA CAGTATTAGC AA - #GCAAAAAA
420
- TGGCCATCAC TAAGGAGCAC TCCATCACTC TTAATCTTAC CATCATGAAT GT - #TTCCCTGC
480
- AAGATTCAGG CACCTATGCC TGCAGAGCCA GGAATGTATA CACAGGGGAA GA - #AATCCTCC
540

551

- (2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:

#pairs (A) LENGTH: 338 base
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

- GAGAGCATCA CTCAGCGCAT GGCAATAATA GAAGGAAAGA ATAAGATGGC TA - #GCACCTTG
60
- GTTGTGGCTG ACTCTAGAAT TTCTGGAATC TACATTTGCA TAGCTTCCAA TA - #AAGTTGGG
120
- ACTGTGGGAA GAAACATAAG CTTTTATATC ACAGAATTGT CAAACTTTGA GT - #GCCTTCAT
180
- CCTTGCTCTC AGGAATAGAA CTCTACCTCA TCGGATCTCA TGTGCCAAAT GG - #GTTTCATG
240
- TTAACCTGGA AAAAATGCCG ACGGAAGGAG AGGACCTGAA ACTGTCTTGC AC - #AGTTAACA
300

338 CGTT ACTTGGATTT TACTGCGG

- (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:

#pairs (A) LENGTH: 358 base
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

- GAGAGCATCA CTCAGCGCAT GGCAATAATA GAAGGAAAGA ATAAGCTTCC AC - #CAGCTGAC
60
- AGTTCTTTCA TGTGCCCACC TACAAGCTTC TCTTCCAAC ACTTCCATTT CC - #TTCCGTGA
120
- CTCTAAACGG ATGGCTAGCA CCTTGGTTGT GGCTGACTCT AGAATTTCTG GA - #ATCTACAT
180
- TTGCATAGCT TCCAATAAAG TTGGGACTGT GGGAAGAAAC ATAAGCTTTT AT - #ATCACAGA

240
 - TGTGCCAAAT GGGTTTCATG TTAACCTGGA AAAAATGCCG ACGGAAGGAG AG - #GACCTGAA
 300
 - ACTGTCTTGC ACAGTTAACA AGTTCTTATA CAGAGACGTT ACTTGGATTT TA - #CTGCGG
 358
 - (2) INFORMATION FOR SEQ ID NO:8:
 - (i) SEQUENCE CHARACTERISTICS:
 #acids (A) LENGTH: 65 amino
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (iii) HYPOTHETICAL: NO
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
 - Glu Ser Ile Thr Gln Arg Met Ala Ile Ile Gl - #u Gly Lys Asn Lys Met
 # 15
 - Ala Ser Thr Leu Val Val Ala Asp Ser Arg Il - #e Ser Gly Ile Tyr Ile
 # 30
 - Cys Ile Ala Ser Asn Lys Val Gly Thr Val Gl - #y Arg Asn Ile Ser Phe
 # 45
 - Tyr Ile Thr Glu Leu Ser Asn Phe Glu Cys Le - #u His Pro Cys Ser Gln
 # 60
 - Glu
 65
 - (2) INFORMATION FOR SEQ ID NO:9:
 - (i) SEQUENCE CHARACTERISTICS:
 #acids (A) LENGTH: 39 amino
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (iii) HYPOTHETICAL: NO
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
 - Glu Ser Ile Thr Gln Arg Met Ala Ile Ile Gl - #u Gly Lys Asn Lys Leu
 # 15
 - Pro Pro Ala Asp Ser Ser Phe Met Leu Pro Pr - #o Thr Ser Phe Ser Ser
 # 30
 - Asn Tyr Phe His Phe Leu Pro
 35
 - (2) INFORMATION FOR SEQ ID NO:10:
 - (i) SEQUENCE CHARACTERISTICS:
 #pairs (A) LENGTH: 19 base
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: other nucleic acid
 #= "PRIMER"A) DESCRIPTION: /desc
 - (iii) HYPOTHETICAL: NO
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
 # 19 TTC
 - (2) INFORMATION FOR SEQ ID NO:11:
 - (i) SEQUENCE CHARACTERISTICS:
 #pairs (A) LENGTH: 20 base
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: other nucleic acid

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#= "PRIMER"A) DESCRIPTION: /desc
-   (iii) HYPOTHETICAL: NO
-   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
# 20          TGTA
- (2) INFORMATION FOR SEQ ID NO:12:
-   (i) SEQUENCE CHARACTERISTICS:
#pairs      (A) LENGTH: 20 base
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear
-   (ii) MOLECULE TYPE: other nucleic acid
#= "PRIMER"A) DESCRIPTION: /desc
-   (iii) HYPOTHETICAL: NO
-   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
# 20          GTTC
- (2) INFORMATION FOR SEQ ID NO:13:
-   (i) SEQUENCE CHARACTERISTICS:
#pairs      (A) LENGTH: 21 base
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear
-   (ii) MOLECULE TYPE: other nucleic acid
#= "PRIMER"A) DESCRIPTION: /desc
-   (iii) HYPOTHETICAL: NO
-   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
#21          CTCA G
- (2) INFORMATION FOR SEQ ID NO:14:
-   (i) SEQUENCE CHARACTERISTICS:
#pairs      (A) LENGTH: 21 base
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear
-   (ii) MOLECULE TYPE: other nucleic acid
#= "PRIMER"A) DESCRIPTION: /desc
-   (iii) HYPOTHETICAL: NO
-   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
#21          ATCC A
- (2) INFORMATION FOR SEQ ID NO:15:
-   (i) SEQUENCE CHARACTERISTICS:
#pairs      (A) LENGTH: 20 base
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear
-   (ii) MOLECULE TYPE: other nucleic acid
#= "PRIMER"A) DESCRIPTION: /desc
-   (iii) HYPOTHETICAL: NO
-   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
# 20          TGTA
- (2) INFORMATION FOR SEQ ID NO:16:
-   (i) SEQUENCE CHARACTERISTICS:
#acids      (A) LENGTH: 14 amino
              (B) TYPE: amino acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear
-   (ii) MOLECULE TYPE: peptide
-   (iii) HYPOTHETICAL: NO
-   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

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- Glu Leu Ser Asn Phe Glu Cys Leu His Pro Cy - #s Ser Gln Glu
10
- (2) INFORMATION FOR SEQ ID NO:17:
- (i) SEQUENCE CHARACTERISTICS:
#acids (A) LENGTH: 24 amino
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:
- Leu Pro Pro Ala Asp Ser Ser Phe Met Leu Pr - #o Pro Thr Ser Phe Ser
15
- Ser Asn Tyr Phe His Phe Leu Pro
20

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